SEQUENCE LISTING

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<110> Broze, George J., Jr.

<120> Protein Z-Dependent Protease Inhibitor

<130> WU-3110/1

<140> 09/271,608
<141> 1999-03-17

<150> US 60/086,571
<151> 1998-05-19

<160> 16

<170> Word Perfect 5.0

<210> 1
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> Xaa=Unknown amino acid
<222> Xaa=Indeterminate residues 10 & 11; can be any amino acid
<223> /note="synthetic construct"

<400> 1
Leu Ala Pro Ser Pro Gln Ser Pro Glu Xaa Xaa Ala
1               5                   10

<210> 2
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> Xaa=Unknown amino acid
<222> Xaa=Indeterminate residue 13; can be any amino acid
<223> /note="synthetic construct"

<400> 2
Arg Tyr Lys Gly Gly Ser Pro Xaa Ile Ser Gln Pro Xaa Leu
1               5                   10

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"
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<400> 3
acccagggta gctttgcctt cat   23

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 4
gtacatcatg ggcaccttaa c   21

<210> 5
<211> 19
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<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 5
Asn Leu Glu Leu Gly Leu Thr Gln Ser Phe Ala Phe Ile His Lys
1   5   10   15

Asp Phe Asp Val

<210> 6
<211> 40
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<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 6
Met Ser Arg Ser Thr Gln Glu Leu Leu Gly Tyr His Cys Arg Leu
1   5   10   15

Gln Asp Lys Leu Gln Glu Gln Glu Gly Ser Leu Ala Ala Glu Gly
                20   25   30

Arg His Ser Leu Ala Ser Ala Ala Asp His
                35   40

<210> 7
<211> 2466
<212> DNA
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<220>

<223> /note="synthetic construct"

<400> 7
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ctggagtggg gtaagaggcg aattatagac acaagggct cctctgcagg        50

aaggaggcca agggaaagag gcttgaaagg cttgatattt cacccaccac       100

cactcactgc cggagtaagc aggtctcccc ttcccagggc tgaggggagg       150

cagggatgtg tgctgtccca gggctgagaa gtggcaggtg agctggtgat       200

tccttactgc ccaggttcgt tctaggaagg tgcgtcctca ccatgctgga       250

tggtgtccta gtccaggagc accccctgag ctcctggcct agactccaaa       300

gggttgggta gatgagcaaa gactttacaa agaccttagg cgatatatgt       350

ccaggagcac ccaggaatta ctgggctacc actgcagact gcaggacaag       400

ctccaagaac aggaaggaag tcttgcagct gaagggaggc actccttggc       450

ctccgcagcc gat cac atg aag gtg gtg cca agt ctc ctg ctc         493
                Met Lys Val Val Pro Ser Leu Leu Leu
                -20                       -15

tcc gtc ctc ctg gca cag gtg tgg ctg gta ccc ggc ttg gcc         535
Ser Val Leu Leu Ala Gln Val Trp Leu Val Pro Gly Leu Ala
       -10                 -5                 -1  1

ccc agt cct cag tcg cca gag acc cca gcc cct cag aac cag         577
Pro Ser Pro Gln Ser Pro Glu Thr Pro Ala Pro Gln Asn Gln
        5                   10                  15

acc agc agg gta gtg cag gct ccc aag gag gaa gag gaa gat         619
Thr Ser Arg Val Val Gln Ala Pro Lys Glu Glu Glu Glu Asp
            20                  25                  30

gag cag gag gcc agc gag gag aag gcc agt gag gaa gag aaa         661
Glu Gln Glu Ala Ser Glu Glu Lys Ala Ser Glu Glu Glu Lys
                35                  40

gcc tgg ctg atg gcc agc agg cag cag ctt gcc aag gag act         703
Ala Trp Leu Met Ala Ser Arg Gln Gln Leu Ala Lys Glu Thr
45                  50                  55

tca aac ttc gga ttc agc ctg ctg cga aag atc tcc atg agg         745
Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile Ser Met Arg
    60                  65                  70

cac gat ggc aac atg gtc ttc tct cca ttt ggc atg tcc ttg         787
His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met Ser Leu
        75                  80                  85
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gcc atg aca ggc ttg atg ctg ggg gcc aca ggg ccg act gaa        829
Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr Glu
        90                      95              100

acc cag atc aag aga ggg ctc cac ttg cag gcc ctg aag ccc        871
Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro
                105                 110

acc aag ccc ggg ctc ctg cct tcc ctc ttt aag gga ctc aga        913
Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg
115             120                 125

gag acc ctc tcc cgc aac ctg gaa ctg ggc ctc aca cag ggg        955
Glu Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Thr Gln Gly
        130             135             140

agt ttt gcc ttc atc cac aag gat ttt gat gtc aaa gag act        997
Ser Phe Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr
        145             150             155

ttc ttc aat tta tcc aag agg tat ttt gat aca gag tgc gtg       1039
Phe Phe Asn Leu Ser Lys Arg Tyr Phe Asp Thr Gly Cys Val
        160             165             170

cct atg aat ttt cgc aat gcc tca cag gcc aaa agg ctc atg       1081
Pro Met Asn Phe Arg Asn Ala Ser Gln Ala Lys Arg Leu Met
                175                 180

aat cat tac att aac aaa gag act cgg ggg aaa att ccc aaa       1123
Asn His Tyr Ile Asn Lys Glu Thr Arg Gly Lys Ile Pro Lys
185             190                 195

ctg ttt gat gag att aat cct gaa acc aaa tta att ctt gtg       1165
Leu Phe Asp Glu Ile Asn Pro Glu Thr Lys Leu Ile Leu Val
        200             205                 210

gat tac atc ttg ttc aaa ggg aaa tgg ttg acc cca ttt gac       1207
Asp Tyr Ile Leu Phe Lys Gly Lys Trp Leu Thr Pro Phe Asp
        215             220                 225

cct gtc ttc acc gaa gtc gac act ttc cac ctg gac aag tac       1249
Pro Val Phe Thr Glu Val Asp Thr Phe His Leu Asp Lys Tyr
            230             235                 240

aag acc att aag gtg ccc atg atg tac ggt gca ggc aag ttt       1291
Lys Thr Ile Lys Val Pro Met Met Tyr Gly Ala Gly Lys Phe
                245             250

gcc tcc acc ttt gac aag aat ttt cgt tgt cat gtc ctc aaa       1333
Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys His Val Leu Lys
255                 260                 265
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```
ctg ccc tac caa gga aat gcc acc atg ctg gtg gtc ctc atg        1375
Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val Val Leu Met
    270             275                 280

gag aaa atg ggt gac cac ctc gcc ctt gaa gac tac ctg acc        1417
Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr Leu Thr
        285             290                 295

aca gac ttg gtg gag aca tgg ctc aga aac atg aaa acc aga        1459
Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr Arg
            300             305                 310

aac atg gaa gtt ttc ttt ccg aag ttc aag cta gat cag aag        1501
Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
                315             320

tat gag atg cat gag ctg ctt agg cag atg gga atc aga aga        1543
Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg
325             330                 335

atc ttc tca ccc ttt gct gac ctt agt gaa ctc tca gct act        1585
Ile Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr
        340             345                 350

gga aga aat ctc caa gta tcc agg gtt tta caa aga aca gtg        1627
Gly Arg Asn Leu Gln Val Ser Arg Val Leu Gln Arg Thr Val
            355             360                 365

att gaa gtt gat gaa agg ggc act gag gca gtg gca gga atc        1669
Ile Glu Val Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile
            370             375                 380

ttg tca gaa att act gct tat tcc atg cct cct gtc atc aaa        1711
Leu Ser Glu Ile Thr Ala Tyr Ser Met Pro Pro Val Ile Lys
                385             390

gtg gac cgg cca ttt cat ttc atg atc tat gaa gaa acc tct        1753
Val Asp Arg Pro Phe His Phe Met Ile Tyr Glu Glu Thr Ser
395             400                 405

gga atg ctt ctg ttt ctg ggc agg gtg gtg aat ccg act ctc        1795
Gly Met Leu Leu Phe Leu Gly Arg Val Val Asn Pro Thr Leu
        410             415                 420

cta taa ttcaggacac gcataagcac ttcgcgtgta gtagatgctg             1841
Leu
423

aatctgaggt atcaaacaca cacaggatac cagcaatgga tggcagggga          1891

gagtgttcct tttgttctta actagtttag ggtgttctca aataaataca          1941

gtagtcccca cttatctgag ggggatacat tcaaagaccc ccagcagatg          1991
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cctgaaacgg tggacagtgc tgaaccttat atatattttt tcctacacat          2041

acatacctat gataaagttt aatttataaa ttaggcacag taagagatta          2091

acaataataa caacattaag taaaatgagt tacttgaatg caagcactgc          2141

ataccataa  cagtcaaact gattatagag aaggctacta agtgactcat          2191

gggcgaggag catagacagt gtggagacat tgggcaaggg gagaattcac          2241

atcctgggtg ggacagagca ggacaatgca agattccatc ccactactca          2291

gaatggcatg ctgcttaaga cttttagatt gtttatttct ggaatttttc          2341

atttaatgtt tttggaccat ggttgaccat ggttaactga gactgcagaa          2391

agcaaaacca tggataaggg aggactacta caaaagcatt aaattgatac          2441

atatttttta aaaaaaaaaa aaaaa                                     2466
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<210> 8
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 8

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Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala
    -20                 -15                 -10

Val Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser
         -5                -1   1                 5

Pro Glu Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val
        10                  15                  20

Gln Ala Pro Lys Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser
             25                  30                  35

Glu Glu Lys Ala Ser Glu Glu Glu Lys Ala Trp Leu Met Ala
             40                  45

Ser Arg Gln Gln Leu Ala Lys Glu Thr Ser Asn Phe Gly Phe
50                  55                  60

Ser Leu Leu Arg Lys Ile Ser Met Arg His Asp Gly Asn Met
    65                  70                  75

Val Phe Ser Pro Phe Gly Met Ser Leu Ala Met Thr Gly Leu
        80                  85                  90
```

```
Met Leu Gly Ala Thr Gly Pro Thr Glu Thr Gln Ile Lys Arg
            95                  100              105

Gly Leu His Leu Gln Ala Leu Lys Pro Thr Lys Pro Gly Leu
            110                 115

Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu Thr Leu Ser Arg
120                 125                 130

Asn Leu Glu Leu Gly Leu Thr Gln Gly Ser Phe Ala Phe Ile
    135                 140                 145

His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn Leu Ser
        150                 155                 160

Lys Arg Tyr Phe Asp Thr Gly Cys Val Pro Met Asn Phe Arg
            165             170                 175

Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
                180             185

Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile
190                 195             200

Asn Phe Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe
    205             210                 215

Lys Gly Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu
        220             225             230

Val Asp Thr Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val
            235             240                 245

Pro Met Met Tyr Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp
                250             255

Lys Asn Phe Arg Cys His Val Leu Lys Leu Pro Tyr Gln Gly
260             265                 270

Asn Ala Thr Met Leu Val Val Leu Met Glu Lys Met Gly Asp
    275             280                 285

His Leu Ala Leu Glu Asp Tyr Leu Thr Thr Asp Leu Val Glu
        290             295                 300

Thr Trp Leu Arg Asn Met Lys Thr Arg Asn Met Glu Val Phe
            305             310                 315

Phe Pro Lys Phe Lys Leu Asp Gln Lys Tyr Glu Met His Glu
                320             325

Leu Leu Arg Gln Met Gly Ile Arg Arg Ile Phe Ser Pro Phe
330             335             340
```

Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg Asn Leu Gln
    345   350   355

Val Ser Arg Val Leu Gln Arg Thr Val Ile Glu Val Asp Glu
    360   365   370

Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
        375   380   385

Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
            390   395

His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe
400   405   410

Leu Gly Arg Val Val Asn Pro Thr Leu Leu
    415   420

<210> 9
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 9

Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
1   5   10   15

Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
            20   25   30

Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu Gly
            35   40   45

Arg Val Val Asn Pro Thr Leu Leu
            50

<210> 10
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 10
Glu Arg Gly Thr Glu Val Val Ser Gly Thr Val Ser Glu Ile Thr
1   5   10   15

```
Ala Tyr Cys Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
                20              25              30

Phe Ile Ile Tyr Glu Glu Met Ser Arg Met Leu Leu Phe Leu Gly
                35              40              45

Arg Val Val Asn Pro Thr Val Leu
                50
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<210> 11
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 11
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Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile
1               5               10              15

Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val
                20              25              30

Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly
                35              40              45

Lys Val Val Asn Pro Thr Gln Lys
                50
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<210> 12
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 12
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Glu Lys Gly Thr Glu Ala Thr Gly Ala Pro His Leu Glu Glu Lys
1               5               10              15

Ala Trp Ser Lys Tyr Gln Thr Val Met Phe Asn Arg Pro Phe Leu
                20              25              30

Val Ile Ile Lys Glu Tyr Ile Thr Asn Phe Pro Leu Phe Ile Gly
                35              40              45

Lys Val Val Asn Pro Thr Gln Lys
                50
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<210> 13
<211> 56
<212> PRT

<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 13
Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala
1   5   10   15

Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe Lys Ala Asn Arg
                20   25   30

Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn Thr Ile Ile
                35   40   45

Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                50   55

<210> 14
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 14
Glu Glu Gly Thr Gln Ala Thr Thr Val Thr Thr Val Gly Phe Met
1   5   10   15

Pro Leu Ser Thr Gln Val Arg Phe Thr Val Asp Arg Pro Phe Leu
                20   25   30

Phe Leu Ile Tyr Glu His Arg Thr Ser Cys Leu Leu Phe Met Gly
                35   40   45

Arg Val Ala Asn Pro Ser Arg Ser
                50

<210> 15
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

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<400> 15
Glu Asp Gly Thr Lys Ala Ser Ala Ala Thr Thr Ala Ile Leu Ile
1               5               10              15


Ala Arg Ser Ser Pro Pro Trp Phe Ile Val Asp Arg Pro Phe Leu
                20              25              30


Phe Phe Ile Arg His Asn Pro Thr Gly Ala Val Leu Phe Met Gly
                35              40              45


Gln Ile Asn Lys Pro
                50



<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 16
Leu Ala Pro Ser Pro Gln Ser Pro Glu Thr Pro Ala
1               5               10
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